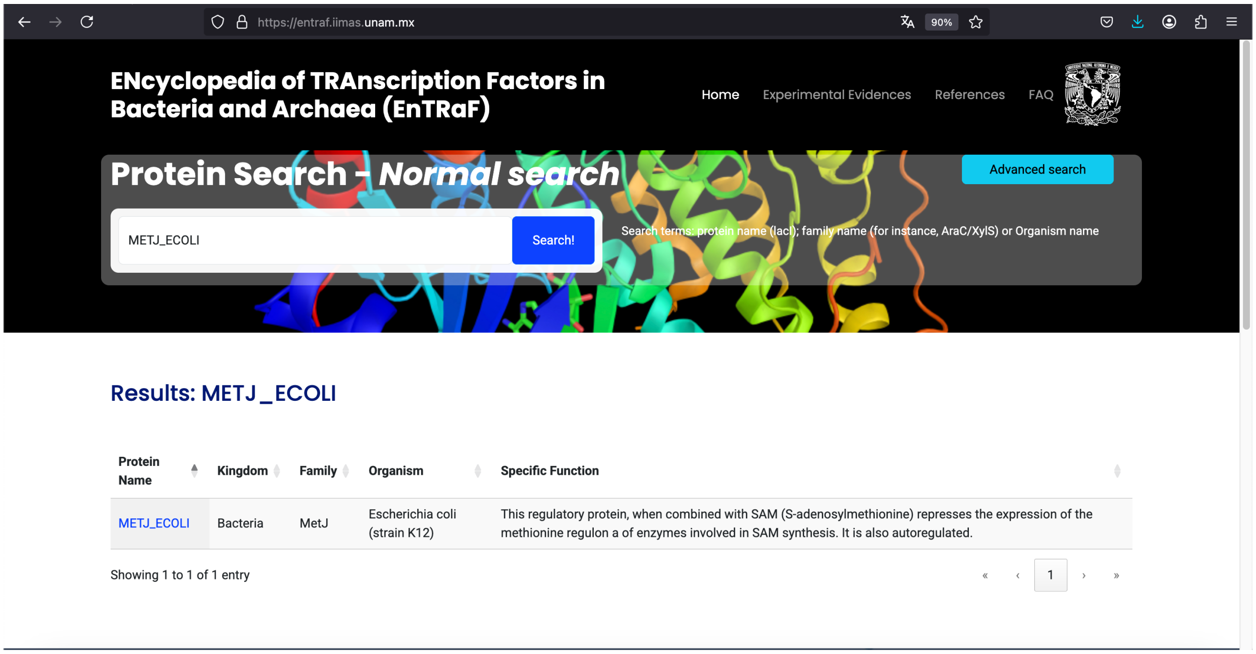
README of ENcyclopedia of TRAnscription Factors in Bacteria and Archaea genomes (ENTRAF) version 2.0.

There are two forms, to search into the database:

1. Input the keyword for the transcription factor: AraC/XylS, MetJ, LacI/GalR or Bacillus subtilis



ENcyclopedia of TRAnscription Factors in Bacteria and Archaea (EnTRaF)

Protein Search - *Normal search*

METJ_ECOLI

Search terms: protein name (lacI); family name (for instance, AraC/XylS) or Organism name

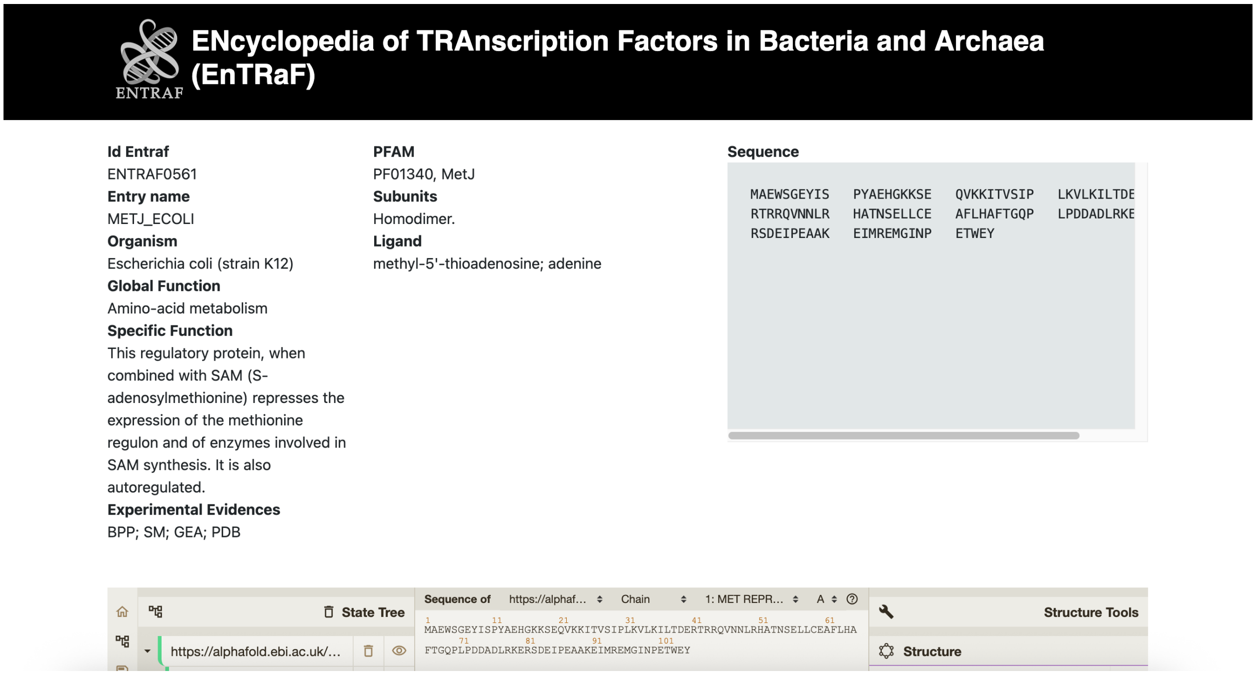
Results: METJ_ECOLI

Protein Name	Kingdom	Family	Organism	Specific Function
METJ_ECOLI	Bacteria	MetJ	Escherichia coli (strain K12)	This regulatory protein, when combined with SAM (S-adenosylmethionine) represses the expression of the methionine regulon a of enzymes involved in SAM synthesis. It is also autoregulated.

Showing 1 to 1 of 1 entry

« ‹ 1 › »

2. Display the Transcription factor (protein) ID



ENcyclopedia of TRAnscription Factors in Bacteria and Archaea (EnTRaF)

Id Entraf
ENTRAF0561
Entry name
METJ_ECOLI
Organism
Escherichia coli (strain K12)
Global Function
Amino-acid metabolism
Specific Function
This regulatory protein, when combined with SAM (S-adenosylmethionine) represses the expression of the methionine regulon and of enzymes involved in SAM synthesis. It is also autoregulated.
Experimental Evidences
BPP; SM; GEA; PDB

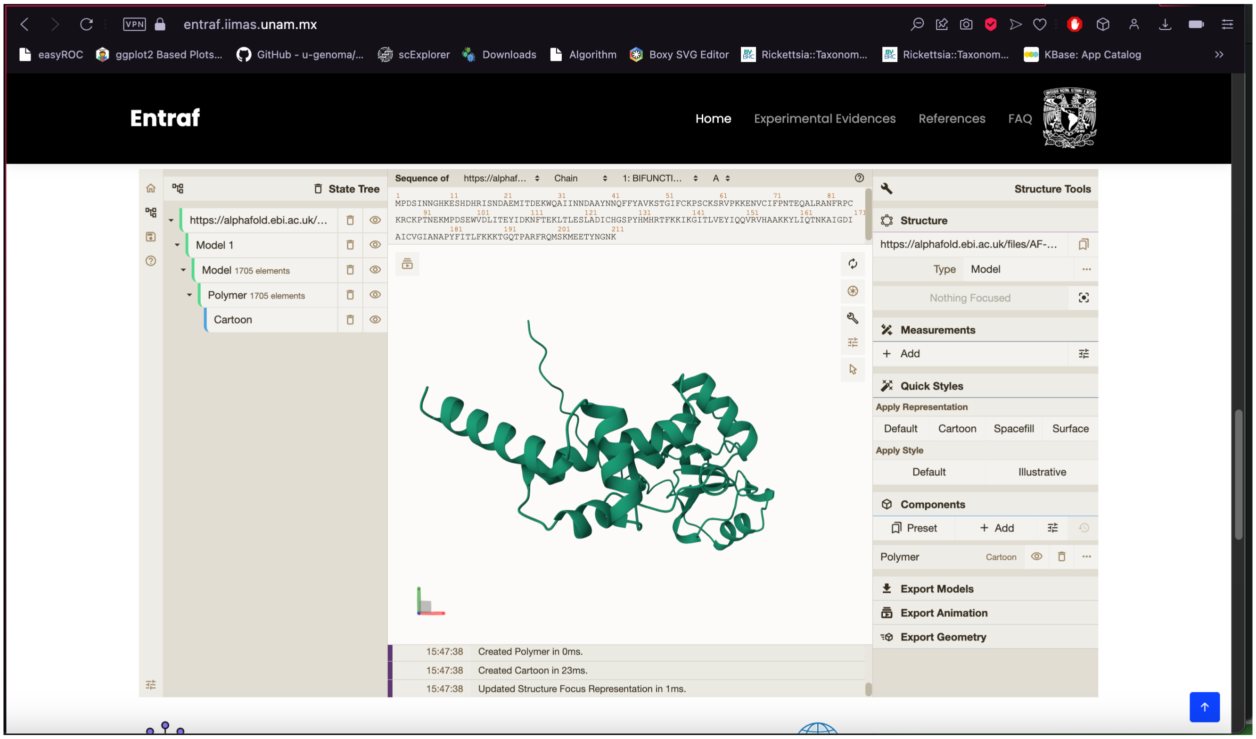
PFAM
PF01340, MetJ
Subunits
Homodimer.
Ligand
methyl-5'-thioadenosine; adenine

Sequence

```
MAEWSGEYIS   PYAEHGKKSE   QVKKITVSIP   LKVLKILTDE
RTRRQVNNLR   HATNSELLCE   AFLHAFTGQP   LPDDADLRKE
RSDEIPEAAK   EIMREMGINP   ETWEY
```

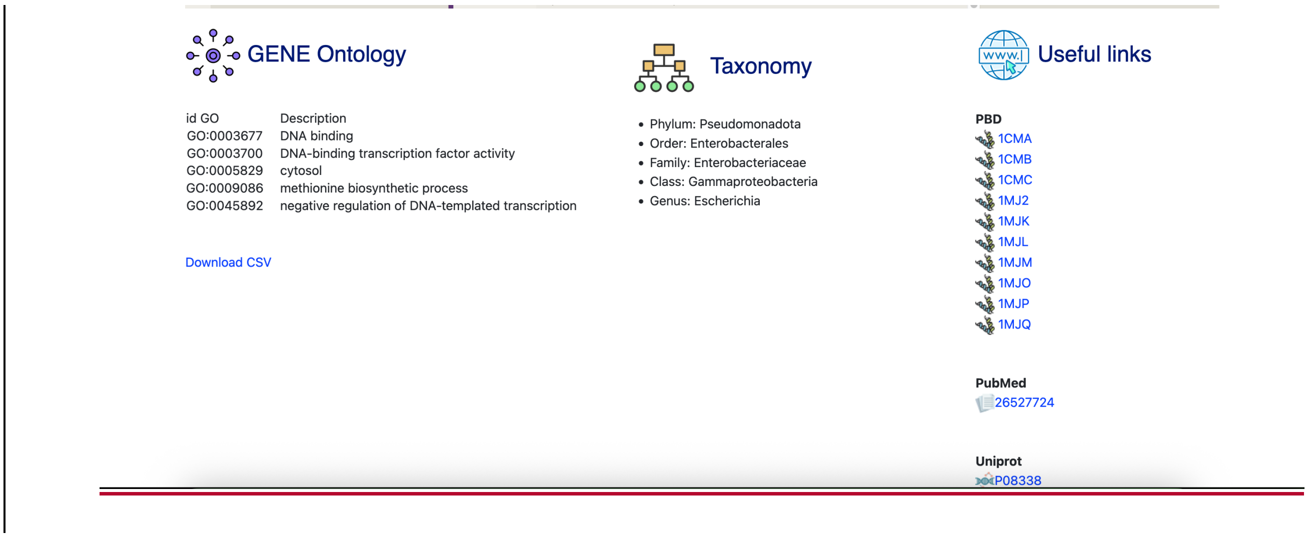
```
1         11        21        31        41        51        61
MAEWSGEYISPYAEHGKKSEQVKKITVSIPLKVLKILTDERTRRQVNNLRHATNSELLCEAFLHA
     71        81        91        101
FTGQPLPDDADLRKERSDEIPEAAKEIMREMGINPETWEY
```

For this entry (MetJ_Ecoli) we display the protein ID (internal database identificator); entry name; Organism; Global function; Specific function; Subunits; Ligand molecule; protein sequence; alpha fold model; Gene ontology; bacterial or archaeal taxonomy and external links to PDB, PubMed and Uniprot databases.



```
1         11        21        31        41        51        61        71        81
MPDSINNGHKESHDHRISNDAEMITDEKWQAIINNDAAYNNQFFYAVKSTGIFCKPSCKSRVPKKENVCIFPNTEQALRANFRPC
     91        101       111       121       131       141       151       161       171
KRCKPTNEKMPDSEWVDLITEYIDKNFTEKLTLESLADICHGSPYHMHRTFKKIKGITLVEYIQQVRVHAAKKYLIQTNKAIGDI
          181       191       201       211
AICVGIANAPYFITLFKKKTGQTPARFRQMSKMEETYNGNK
```

```
15:47:38   Created Polymer in 0ms.
15:47:38   Created Cartoon in 23ms.
15:47:38   Updated Structure Focus Representation in 1ms.
```



GENE Ontology

id GO	Description
GO:0003677	DNA binding
GO:0003700	DNA-binding transcription factor activity
GO:0005829	cytosol
GO:0009086	methionine biosynthetic process
GO:0045892	negative regulation of DNA-templated transcription

Download CSV

Taxonomy

- Phylum: Pseudomonadota
- Order: Enterobacterales
- Family: Enterobacteriaceae
- Class: Gammaproteobacteria
- Genus: Escherichia

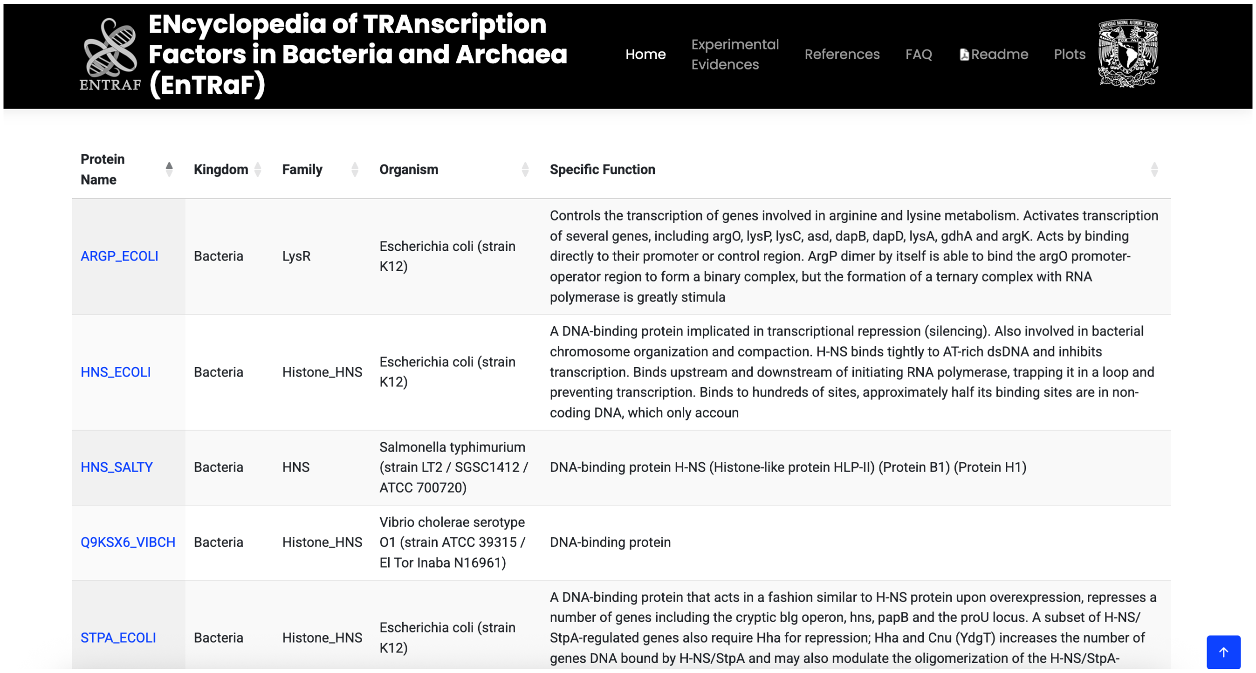
Useful links

PBD
1CMA
1CMB
1CMC
1MJ2
1MJK
1MJL
1MJM
1MJO
1MJP
1MJQ

PubMed
26527724

Uniprot
P08338

1. Alternatively, for advance searches; we included diverse fields to be considered: Gene ontology; Global regulation and/or taxonomy. For instance, for the term “bent DNA-binding”, we get the following result:



Protein Name	Kingdom	Family	Organism	Specific Function
ARGP_ECOLI	Bacteria	LysR	Escherichia coli (strain K12)	Controls the transcription of genes involved in arginine and lysine metabolism. Activates transcription of several genes, including argO, lysP, lysC, asd, dapB, dapD, lysA, gdhA and argK. Acts by binding directly to their promoter or control region. ArgP dimer by itself is able to bind the argO promoter-operator region to form a binary complex, but the formation of a ternary complex with RNA polymerase is greatly stimula
HNS_ECOLI	Bacteria	Histone_HNS	Escherichia coli (strain K12)	A DNA-binding protein implicated in transcriptional repression (silencing). Also involved in bacterial chromosome organization and compaction. H-NS binds tightly to AT-rich dsDNA and inhibits transcription. Binds upstream and downstream of initiating RNA polymerase, trapping it in a loop and preventing transcription. Binds to hundreds of sites, approximately half its binding sites are in non-coding DNA, which only accoun
HNS_SALTY	Bacteria	HNS	Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)	DNA-binding protein H-NS (Histone-like protein HLP-II) (Protein B1) (Protein H1)
Q9KSX6_VIBCH	Bacteria	Histone_HNS	Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)	DNA-binding protein
STPA_ECOLI	Bacteria	Histone_HNS	Escherichia coli (strain K12)	A DNA-binding protein that acts in a fashion similar to H-NS protein upon overexpression, represses a number of genes including the cryptic blg operon, hns, papB and the proU locus. A subset of H-NS/StpA-regulated genes also require Hha for repression; Hha and Cnu (YdgT) increases the number of genes DNA bound by H-NS/StpA and may also modulate the oligomerization of the H-NS/StpA-

And as in the original search, the protein record can be displayed to check all the functional information.